

0405 0300 #3



OIPF

RAW SEQUENCE LISTING

DATE: 02/07/2002

PATENT APPLICATION: US/10/041,778

TIME: 18:26:50

Input Set : N:\Crf3\RULE60\10041778.txt

Output Set: N:\CRF3\02072002\J041778.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Bowman, Michael

8 (ii) TITLE OF INVENTION: SECRETED PROTEIN BA3.1 AND

9 POLYNUCLEOTIDES ENCODING SAME

11 (iii) NUMBER OF SEQUENCES: 2

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Genetics Institute, Inc.

15 (B) STREET: 87 CambridgePark Drive

16 (C) CITY: Cambridge

17 (D) STATE: Massachusetts

18 (E) COUNTRY: U.S.A.

19 (F) ZIP: 02140

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/10/041,778

C--> 29 (B) FILING DATE: 07-Jan-2002

35 (C) CLASSIFICATION:

32 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: 09/041,159

34 (B) FILING DATE: 03-DEC-1998

38 (viii) ATTORNEY/AGENT INFORMATION:

39 (A) NAME: Sprunger, Suzanne A.

40 (B) REGISTRATION NUMBER: 41,323

41 (C) REFERENCE/DOCKET NUMBER: GI5295A

43 (ix) TELECOMMUNICATION INFORMATION:

44 (A) TELEPHONE: (617) 498-8284

45 (B) TELEFAX: (617) 876-5851

48 (2) INFORMATION FOR SEQ ID NO: 1:

50 (i) SEQUENCE CHARACTERISTICS:

51 (A) LENGTH: 1086 base pairs

52 (B) TYPE: nucleic acid

53 (C) STRANDEDNESS: double

54 (D) TOPOLOGY: linear

56 (ii) MOLECULE TYPE: cDNA

61 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

63	GCGGCGGTAC GATTTGTTAG ACACAGGAGA TGATCTTGAC CCTGATATCA TTAATATCCT	60
65	TCCTGCTTCT CCAACTGGTT CTCCTGTACA TTCTCCAGGA TCTCATTACC CCCATGGAGG	120
67	TGATGCGGGC AAGGGTCAGA GTACTGATCG GCTACTATCA ACAGAACCTC ATGAGGAAGT	180

ENTERED

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69 ACCTAATATT CTTCAAGCAAC CATTGGCCCT TGGTTACTTT GTATCAACTG CCAAAGCAGG      240
71 TCCATTACCT GACTGGTTCT GGTCAAGCATG TCCTCAAGCA CAATATCAGT GTCCCCTTTT      300
73 TTCTTAAGGC CTCTTTGCAC CTCCACGTGC CTTCAAGTGA ATCTGACGAG CTGCTTCACA      360
75 GTAAACACTC CCACCCACTT GACTCAAATC AGACTTCAGA TGTCCTCAGG TTTGTTTTTG      420
77 AACAGTACAA TGCACCTCTCC TGGCTAACCT GTGACCCTGC AACCCAGGAC AGACGCTCAT      480
79 GTCTCCCAAT TCATTTTGTG GTGCTGAATC AGTTATATAA CTTTATTATG AATATGCTGT      540
81 GATCTTCATT TGATGGAAC TGTCAAGAAA AGAACAAGGA AAAATGGATG TTTGCTGCA      600
83 GGATTAAGTT ACAATTATCT TCTCAGTGAA GGTCATTTGT GATGGGGTCT AATTCTTATT      660
85 ACTTCAACAA ATATTGTTTT GACTTGGGGG GAGGGGCTAT AACCTGCTA TTTTTCATTG      720
87 ACTCTATTGA ACTCTTAGG ATGATGACTG ATCATAAAA ACGTATTATA ACATTTTCGT      780
89 AGCAAAATTA ACCTTTTTTT TTTCCAGTCA CAGTATTTGT GAAAAGTAAT GAGCCATAGT      840
91 ACCCAGTCAT GTTAAATGAA TATTAAGAGC ATGGAGAGGA AACATGAGGA ACAATGAATT      900
93 TCAACATATG GCTTCAGAAC ATGAAGATGT TCTTGTATGG ATTATAGTAT CTAGTATTCA      960
95 AAAATGCCTG CATCTCTTCT CTTATTTATT GTAAGTTTTT AAATGTATAA ATTGTCTTAT     1020
97 ATTTCTTAAC CTCTTTTATA AAAATTTTCC TAGAAGGTTT ATACTGCCAA AAAAAAAAAA     1080
99 AAAAAA                                           1086

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101 (2) INFORMATION FOR SEQ ID NO: 2:

103 (i) SEQUENCE CHARACTERISTICS:

104 (A) LENGTH: 170 amino acids

105 (B) TYPE: amino acid

106 (C) STRANDEDNESS:

107 (D) TOPOLOGY: linear

109 (ii) MOLECULE TYPE: protein

114 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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116 Met Ile Leu Thr Leu Ile Ser Leu Ile Ser Phe Leu Leu Leu Gln Leu
117 1 5 10 15
119 Val Leu Leu Tyr Ile Leu Gln Asp Leu Ile Thr Pro Met Glu Val Met
120 20 25 30
122 Arg Ala Arg Val Arg Val Leu Ile Gly Tyr Tyr Gln Gln Asn Leu Met
123 35 40 45
125 Arg Lys Tyr Leu Ile Phe Phe Ser Asn His Trp Pro Leu Val Thr Leu
126 50 55 60
128 Tyr Gln Leu Pro Lys Gln Val His Tyr Leu Thr Gly Ser Gly Gln His
129 65 70 75 80
131 Val Leu Lys His Asn Ile Ser Val Pro Phe Phe Leu Lys Ala Ser Leu
132 85 90 95
134 His Leu His Val Pro Ser Val Gln Ser Asp Glu Leu Leu His Ser Lys
135 100 105 110
137 His Ser His Pro Leu Asp Ser Asn Gln Thr Ser Asp Val Leu Arg Phe
138 115 120 125
140 Val Leu Glu Gln Tyr Asn Ala Leu Ser Trp Leu Thr Cys Asp Pro Ala
141 130 135 140
143 Thr Gln Asp Arg Arg Ser Cys Leu Pro Ile His Phe Val Val Leu Asn
144 145 150 155 160
146 Gln Leu Tyr Asn Phe Ile Met Asn Met Leu
147 165 170

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VERIFICATION SUMMARY

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]